methods for making said products are materially coupled and do not constitute distinct inventions within the meaning proscribed in MPEP § 806.05. Moreover, the close relationship of the subject matter of these groups clearly obviates the need for separate searching and examination by the Office, and coordinate examination of these groups would fulfill the Office's goal of compact prosecution while relieving Applicants of the burden that would attend strict application of the foregoing restriction requirement.

Applicant reserves the right to file a divisional or related application to the claims of non-elected group(s).

AMENDMENT

Please amend the application as follows:

In the Claims

Please cancel claim 95 without prejudice.

Please amend claim 100 as follows:

100. (Amended) The isolated infectious PIV particle of claim 91, wherein the [counterpart gene or gene segment is a gene or gene segment of the] recombinant PIV genome or antigenome has one or more HPIV3 HN or F glycoprotein [gene of] genes or gene segments substituted by one or more counterpart HPIV1 or HPIV2 genes or gene segments.

Please add new claims 129-143 as follows:

--129. The isolated polynucleotide molecule of claim 4, wherein the HN and F glycoprotein genes of HPIV1 are substituted for the counterpart HN and F glycoprotein genes of HPIV3 to encode a chimeric genome or antigenome.

130. The isolated polynucleotide molecule of claim 129, wherein the isolated polynucleotide encoding the chimeric PIV genome or antigenome further incorporates one or more mutations of JS *cp*45.

131. The isolated polynucleotide molecule of claim 130, wherein said one or more mutations of JS *cp*45 comprise a plurality and up to a full complement of mutations present in JS *cp*45.

132. The isolated polynucleotide molecule of claim 129, wherein the isolated polynucleotide encoding the chimeric PIV genome or antigenome further incorporates a full complement of mutations present in JS *cp*45, said full complement of mutations comprising i) substitutions specifying a replacement of His for Tyr_{942}, Phe for Leu_{992}, and Ile for Thr_{1558} in the polymerase L protein; ii) substitutions specifying a replacement of Ala for Val_{96} and Ala for Ser_{389} in the N protein; iii) a substitution specifying a replacement of Thre for Ile_{96} in the C protein; iv) substitution specifying an amino acid change in the F protein comprising a replacement of Val for Ile_{420} or Thr for Ala_{450}; v) substitutions specifying a replacement of Ala for Val_{384} in the HN protein; vi) a substitution specifying a replacement of Thr for Pro_{199} in the M protein; vii) mutations in a 3′ leader sequence comprising a T to C change at a position corresponding to nucleotide 23 of JS *cp*45, a C to T change at nucleotide 24, a G to T change at nucleotide 28, and a T to A change at nucleotide 45 of JS *cp*45; and viii) a mutation in an N gene start sequence comprising an A to T change at a position corresponding to nucleotide 62 of JS *cp*45.

133. The isolated polynucleotide molecule of claim 36, wherein the HN and F glycoprotein genes of HPIV1 are substituted for the counterpart HN and F glycoprotein genes of HPIV3.

134. The isolated polynucleotide molecule of claim 133, wherein said chimeric genome or antigenome incorporates a full complement of mutations present in JS

*cp*45, said full complement of mutations comprising i) substitutions specifying a replacement of His for Tyr_{942}, Phe for Leu_{992}, and Ile for Thr_{1558} in the polymerase L protein; ii) substitutions specifying a replacement of Ala for Val_{96} and Ala for Ser_{389} in the N protein; iii) a substitution specifying a replacement of Thre for Ile_{96} in the C protein; iv) substitution specifying an amino acid change in the F protein comprising a replacement of Val for Ile_{420} or Thr for Ala_{450}; v) substitutions specifying a replacement of Ala for Val_{384} in the HN protein; vi) a substitution specifying a replacement of Thr for Pro_{199} in the M protein; vii) mutations in a 3′ leader sequence comprising a T to C change at a position corresponding to nucleotide 23 of JS *cp*45, a C to T change at nucleotide 24, a G to T change at nucleotide 28, and a T to A change at nucleotide 45 of JS *cp*45; and viii) a mutation in an N gene start sequence comprising an A to T change at a position corresponding to nucleotide 62 of JS *cp*45.

135. The method of claim 81, wherein the HN and F glycoprotein genes of HPIV1 are substituted for the counterpart HN and F glycoprotein genes of HPIV3.

136. The method of claim 135, wherein said genome or antigenome incorporates a full complement of mutations present in JS *cp*45, said full complement of mutations comprising i) substitutions specifying a replacement of His for Tyr_{942}, Phe for Leu_{992}, and Ile for Thr_{1558} in the polymerase L protein; ii) substitutions specifying a replacement of Ala for Val_{96} and Ala for Ser_{389} in the N protein; iii) a substitution specifying a replacement of Thre for Ile_{96} in the C protein; iv) substitution specifying an amino acid change in the F protein comprising a replacement of Val for Ile_{420} or Thr for Ala_{450}; v) substitutions specifying a replacement of Ala for Val_{384} in the HN protein; vi) a substitution specifying a replacement

of Thr for Pro_{199} in the M protein; vii) mutations in a 3' leader sequence comprising a T to C change at a position corresponding to nucleotide 23 of JS *cp*45, a C to T change at nucleotide 24, a G to T change at nucleotide 28, and a T to A change at nucleotide 45 of JS *cp*45; and viii) a mutation in an N gene start sequence comprising an A to T change at a position corresponding to nucleotide 62 of JS *cp*45.

137. The isolated infectious PIV particle of claim 97, wherein HN and F glycoprotein genes of HPIV1 are substituted for counterpart HN and F glycoprotein genes of HPIV3.

138. The isolated infectious PIV particle of claim 137, wherein the recombinant PIV genome or antigenome further incorporates one or more mutations of JS *cp*45.

139. The isolated infectious PIV particle of claim 138, wherein said one or more mutations of JS *cp*45 comprise a plurality and up to a full complement of mutations present in JS *cp*45.

140. The isolated infectious PIV particle of claim 137, wherein the isolated polynucleotide encoding the chimeric PIV genome or antigenome further incorporates a full complement of mutations present in JS *cp*45, said full complement of mutations comprising i) substitutions specifying a replacement of His for Tyr_{942}, Phe for Leu_{992}, and Ile for Thr_{1558} in the polymerase L protein; ii) substitutions specifying a replacement of Ala for Val_{96} and Ala for Ser_{389} in the N protein; iii) a substitution specifying a replacement of Thre for Ile_{96} in the C protein; iv) substitution specifying an amino acid change in the F protein comprising a replacement of Val for Ile_{420} or Thr for Ala_{450}; v) substitutions specifying a replacement of Ala for

Val_{384} in the HN protein; vi) a substitution specifying a replacement of Thr for Pro_{199} in the M protein; vii) mutations in a 3′ leader sequence comprising a T to C change at a position corresponding to nucleotide 23 of JS *cp*45, a C to T change at nucleotide 24, a G to T change at nucleotide 28, and a T to A change at nucleotide 45 of JS *cp*45; and viii) a mutation in an N gene start sequence comprising an A to T change at a position corresponding to nucleotide 62 of JS *cp*45.

141. The isolated infectious PIV particle of claim 111, wherein said chimeric PIV genome or antigenome further incorporates the full complement of mutations present in JS *cp*45, said full complement of mutations comprising i) substitutions specifying a replacement of His for Tyr_{942}, Phe for Leu_{992}, and Ile for Thr_{1558} in the polymerase L protein; ii) substitutions specifying a replacement of Ala for Val_{96} and Ala for Ser_{389} in the N protein; iii) a substitution specifying a replacement of Thre for Ile_{96} in the C protein; iv) substitution specifying an amino acid change in the F protein comprising a replacement of Val for Ile_{420} or Thr for Ala_{450}; v) substitutions specifying a replacement of Ala for Val_{384} in the HN protein; vi) a substitution specifying a replacement of Thr for Pro_{199} in the M protein; vii) mutations in a 3′ leader sequence comprising a T to C change at a position corresponding to nucleotide 23 of JS *cp*45, a C to T change at nucleotide 24, a G to T change at nucleotide 28, and a T to A change at nucleotide 45 of JS *cp*45; and viii) a mutation in an N gene start sequence comprising an A to T change at a position corresponding to nucleotide 62 of JS *cp*45.

142. The immunogenic composition of claim 124, wherein the HN and F glycoprotein genes of HPIV1 are